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* You should state whether an appropriate sample size was computed when the study was being designed
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* You should include a definition of biological versus technical replication
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* Statistical analysis methods should be described and justified
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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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Not applicable.

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
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Raw barcode sequencing data are available from the NIH Sequence Read Archive as accession PRJNA630095 (<https://trace.ncbi.nlm.nih.gov/Traces/study/?acc=SRP259652>). Barcode sequences, counts, fitness values, and PPI calls are available in the Supplementary Tables (<https://osf.io/jmhrb/>). Additional data to make figures are available in Mendeley data (<https://data.mendeley.com/datasets/9ygwhk5cs3/2>) and Open Science Framework (<https://osf.io/7yt59/>) as detailed in code repository README files. Analysis scripts are written in R and Python. All code used to analyze data, perform statistical analyses, and generate figures is available at Github (<https://github.com/sashaflevy/PPiSeq>).